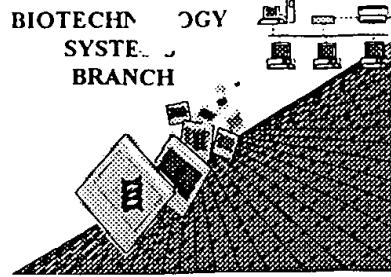


Sorbe 10

HV
7-26-01
P.2

RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/515, 369 A

RECEIVED

Source: 16 33

JUL 25 2001

Date Processed by STIC: 7-5-01

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be downloaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

RECEIVED

JUL 25 2001

Raw Sequence Listing Error Summary

TECH CENTER 1600/2900

ERROR DETECTED SUGGESTED CORRECTION SERIAL NUMBER: 09/515, 369A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleic
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (ii) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 Use of <220>
 "bug" Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/515,369A

DATE: 07/05/2001

TIME: 12:54:49

Input Set : A:\56778.txt

Output Set: N:\CRF3\07032001\I515369A.raw

3 <110> APPLICANT: Fisher, Paul
 4 Madireddi, Malavi
 6 <120> TITLE OF INVENTION: MELANOMA DIFFERENTIATION ASSOCIATED GENE-7 PROMOTER AND USES
 THEREOF
 8 <130> FILE REFERENCE: 0575/56778/JPW/APE
 10 <140> CURRENT APPLICATION NUMBER: 09/515,369A
 11 <141> CURRENT FILING DATE: 2000-02-29
 13 <160> NUMBER OF SEQ ID NOS: 13
 15 <170> SOFTWARE: PatentIn version 3.0
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 2286
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Human
 22 <400> SEQUENCE: 1

23	taatacgaact cactataggg cgtcgactcg atcacctttt gaacccaggt ctgcctgcct	60
25	ccaaagcttg tactcataac tagattctca actgtatgtt gccaagggtt cctaggttct	120
27	ctccttgacc ttcccttctga agtaataatg ctatgataag ctcatacgag gctgaggccc	180
29	aggcacatgt ttgcctgaac tatccatgtt atatgattcc ttccctcagac agagttagct	240
31	actcacgatc ccaggtgtac cctgaggcca gccaagggtt atccatgacc tcatacctct	300
33	gttccagcc gcccatttaac agtcataccc acctgcctgc cttcccccgc tatctgcaga	360
35	cagtagtcta ggatttcage tggccctgggg gtcattttc cctctcagct ttctgtttta	420
37	gctgtctcct gcctcccaact caccttattac tccagcaact tcacctggc ttctttctg	480
39	tctcatcaact gcctcttgac atctttatct catagtagtt agtttaggggt tcttggtaat	540
41	gccctaaatc cacatgggtt gaaggggggg gtggggaaag agagtgcgt gtggggctgt	600
43	gctacttct ggagggttaag actcgggccc tccagaaca aaggattcag gctggggca	660
45	gctatagcca agcagactgc tggccaggga ttgcaaaggaa gtattttgt tgcttaagaa	720
47	aataaaacaac actgagatag agatggaggg aggggggtt ggtgccagag agattggaa	780
49	gagtctgcca agggtgtt ctactcaact tcctttttc ttcatctcc actgagctgg	840
51	aggcagttat cctgtcccc acgtcacatt cctactcccg tttcccatgc ctggacccag	900
53	gttgggcaaa ctcttctgtt aaagaaccag acaggaacta ttttaggctc tgtgtccat	960
55	atggtctcag tcacaactac tcatactctgc ctctgttagca cgaaagcaat tagcaacaat	1020
57	atgtcaacaa acatatgtga ccccatgaaa actttatata ttatggatac ggaaacctga	1080
59	aaataatgtc ttttttttga ttttttcccc aatcattaaa aaacgtaaaaa actacttta	1140
61	ggtcgcaagg ttaagccatt ctcaagttttag cagtgcagg ctggatattgg cttgtgacct	1200
63	acagttggcc aatccctgtat tcccaaaaatg tattctcag ggatgtgggc aaataacttat	1260
65	gggaagtgtt ggattaaaca gagttaaaga gcatcagaca tttccaggac gggctagcac	1320
67	atgccaggc tctctaactg acctcattgg attcatctgt ttcatggagg atcttgcaag	1380
69	acaagaattc ctcaaaccata gagtctgagg actgtgtttt gggaaacact gctctgttt	1440
71	atgccctcac tgggcacatg gtataaatcta gagctgagtg cttgtctagc tggagatagg	1500
73	gtcagagctc ttgactgccc tgcagttt gacacatcac gctgtctgt tcccctgagt	1560
75	ggttcagagc cacacaggcc aagactagcc caccagagca ccaggcctcc cagctttctg	1620
77	ggcttgcata tgcgtacatt tccttattct tcctgtttc cagaacctaa ggagaggcac	1680
79	attttggttt agtgattata acccttaggaa ccatgggtt gtcgtatgtca ggaaacactc	1740
81	ctcaacttcc tggccctgtat ggattaaagg agaggtactt acaggttatt tcttcgtgt	1800
83	ggactactgt cccagcatga atagggcattt attattgaat tattttgaca ggaaggagac	1860
85	tgggttatgc tgcacagtaa taatgttattt acatgtgtac agagtttacc aagcacctct	1920
87	gtgttggttt tgccttggattt tattacactt gggacaaatt tttaaaattt atacatgcag	1980
89	agactgcago gcagagaagc taagagactt gcccctgccc acacagccag tggtagagcc	2040

Does Not Comply
 Corrected Diskette Needed

See p. 4

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/515,369A

DATE: 07/05/2001

TIME: 12:54:49

Input Set : A:\56778.txt

Output Set: N:\CRF3\07032001\I515369A.raw

91	tgaactcaaa cccaggtctc attcacacc aggggctgct ttccccatcg ctgtattgtc	2100
93	cttaaagtga tgggtgacta ggcaatgaag taattctcta gaaaagcatg accaatttcc	2160
95	ctttctccac ctcccctttt ttcctccacc cctccccat cagccccat atatatgcc	2220
97	aatctccac aaagccttgc ttgcctgcaa accttactt ctgaaatgac ttccacggct	2280
99	gggacg	2286
102	<210> SEQ ID NO: 2	
103	<211> LENGTH: 21	
104	<212> TYPE: DNA	
105	<213> ORGANISM: Artificial Sequence	
107	<220> FEATURE:	
108	<221> NAME/KEY: misc_feature	
109	<222> LOCATION: ()..()	
110	<223> OTHER INFORMATION: primer	
113	<400> SEQUENCE: 2	
114	cgtcccagcc gtggaaagtca t	21
117	<210> SEQ ID NO: 3	
118	<211> LENGTH: 21	
119	<212> TYPE: DNA	
120	<213> ORGANISM: Artificial Sequence	
122	<220> FEATURE:	
123	<221> NAME/KEY: misc_feature	
124	<222> LOCATION: ()..()	
125	<223> OTHER INFORMATION: primer	
128	<400> SEQUENCE: 3	
129	aggctggatt tggcttgtga c	21
132	<210> SEQ ID NO: 4	
133	<211> LENGTH: 21	
134	<212> TYPE: DNA	
135	<213> ORGANISM: Artificial Sequence	
137	<220> FEATURE:	
138	<221> NAME/KEY: misc_feature	
139	<222> LOCATION: ()..()	
140	<223> OTHER INFORMATION: primer	
143	<400> SEQUENCE: 4	
144	ctgttaatc cagcaattcc c	21
147	<210> SEQ ID NO: 5	
148	<211> LENGTH: 21	
149	<212> TYPE: DNA	
150	<213> ORGANISM: Artificial Sequence	
152	<220> FEATURE:	
153	<221> NAME/KEY: misc_feature	
154	<222> LOCATION: ()..()	
155	<223> OTHER INFORMATION: primer	
158	<400> SEQUENCE: 5	
159	cgcttgatga ctcagccgga a	21
162	<210> SEQ ID NO: 6	
163	<211> LENGTH: 20	
164	<212> TYPE: DNA	
165	<213> ORGANISM: Artificial Sequence	

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/515,369A

DATE: 07/05/2001

TIME: 12:54:49

Input Set : A:\56778.txt

Output Set: N:\CRF3\07032001\I515369A.raw

167 <220> FEATURE:
168 <221> NAME/KEY: misc_feature
169 <222> LOCATION: ()..()
170 <223> OTHER INFORMATION: primer
173 <400> SEQUENCE: 6
174 tgcagattgc gcaatctgca 20
177 <210> SEQ ID NO: 7
178 <211> LENGTH: 21
179 <212> TYPE: DNA
180 <213> ORGANISM: Artificial Sequence
182 <220> FEATURE:
183 <221> NAME/KEY: misc_feature
184 <222> LOCATION: ()..()
185 <223> OTHER INFORMATION: primer
188 <400> SEQUENCE: 7
189 cgcttgatga cttggccgga a 21
192 <210> SEQ ID NO: 8
193 <211> LENGTH: 22
194 <212> TYPE: DNA
195 <213> ORGANISM: Artificial Sequence
197 <220> FEATURE:
198 <221> NAME/KEY: misc_feature
199 <222> LOCATION: ()..()
200 <223> OTHER INFORMATION: primer
203 <400> SEQUENCE: 8
204 tgcagagaga cttagtctctg ca 22
207 <210> SEQ ID NO: 9
208 <211> LENGTH: 61
209 <212> TYPE: DNA
210 <213> ORGANISM: Artificial Sequence
212 <220> FEATURE:
213 <221> NAME/KEY: misc_feature
214 <222> LOCATION: ()..()
215 <223> OTHER INFORMATION: primer
218 <400> SEQUENCE: 9
219 uuguauuuau uacaacucua uuuauuuau gucaguauuu caacugaagu ucuauuuauu 60
221 u 61
224 <210> SEQ ID NO: 10
225 <211> LENGTH: 15
226 <212> TYPE: DNA
227 <213> ORGANISM: Artificial Sequence
229 <220> FEATURE:
230 <221> NAME/KEY: misc_feature
231 <222> LOCATION: ()..()
232 <223> OTHER INFORMATION: primer
235 <400> SEQUENCE: 10
236 uauuuauuuua uuuua 15
239 <210> SEQ ID NO: 11
240 <211> LENGTH: 51

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/515,369A

DATE: 07/05/2001
TIME: 12:54:49

Input Set : A:\56778.txt
Output Set: N:\CRF3\07032001\I515369A.raw

241 <212> TYPE: DNA		
242 <213> ORGANISM: Artificial Sequence		
244 <220> FEATURE:		
245 <221> NAME/KEY: misc_feature		
246 <222> LOCATION: ()..()		
247 <223> OTHER INFORMATION: primer		
250 <400> SEQUENCE: 11		
251 uaaaauuuaau aaauuuauau uuuuaaaaua uuuauuuauu uauuuauuuua a		51
254 <210> SEQ ID NO: 12		
255 <211> LENGTH: 38		
256 <212> TYPE: DNA		
257 <213> ORGANISM: Artificial Sequence		
259 <220> FEATURE:		
260 <221> NAME/KEY: misc_feature		
261 <222> LOCATION: ()..()		
262 <223> OTHER INFORMATION: primer		
265 <400> SEQUENCE: 12		
W--> 266 suncauuauu uauuuuuauu uuauuuuuua uuuauuuua		38
269 <210> SEQ ID NO: 13		
270 <211> LENGTH: 56		
271 <212> TYPE: DNA		
272 <213> ORGANISM: Artificial Sequence		
274 <220> FEATURE:		
275 <221> NAME/KEY: misc_feature		
276 <222> LOCATION: ()..()		
277 <223> OTHER INFORMATION: primer		
280 <400> SEQUENCE: 13		
281 guuuuuuaauu uauuuauuaa gauggauucu cagauuuua uauuuuuauu uuaauu		56

Sequence #12 is missing the mandatory <220> to <223> features to explain the "n" in the sequence. See #9 on the Error Summary Sheet.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/515,369A

DATE: 07/05/2001

TIME: 12:54:50

Input Set : A:\56778.txt

Output Set: N:\CRF3\07032001\I515369A.raw

L:266 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12